

SEQUENCE LISTING

<110> MIYATA, Toshio
KUROKAWA, Kiyoshi

<120> Meg-3 protein

<130> 2605/101

<140> 10/018,311

<141> 2000-4-28

<160> 8

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 3768

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 3395, 3437, and 3440

<223> N=G,A,C or T

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Met Gly
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Trp Met Gly Glu Lys Thr Gly Lys Ile Leu Thr Glu Phe Leu Gln Phe
5 10 15

tat gaa gac cag tat ggc gtg gct ctc ttc aac agc atg cgc cat gag 154
Tyr Glu Asp Gln Tyr Gly Val Ala Leu Phe Asn Ser Met Arg His Glu
20 25 30

att gag ggc acg ggg ctg ccg cag gcc cag ctg ctc tgg cgc aag gtg 202
Ile Glu Gly Thr Gly Leu Pro Gln Ala Gln Leu Leu Trp Arg Lys Val
35 40 45 50

cca ctg gac gag cgc atc gtc ttc tcg ggg aac ctc ttc cag cac cag 250
Pro Leu Asp Glu Arg Ile Val Phe Ser Gly Asn Leu Phe Gln His Gln
55 60 65

gag gac agc aag aag tgg aga aac cgc ttc agc ctc gtg ccc cac aac 298
Glu Asp Ser Lys Lys Trp Arg Asn Arg Phe Ser Leu Val Pro His Asn
70 75 80

tac ggg ctg gtg ctc tac gaa aac aaa gcc gcc tat gag cgg cag gtc 346
Tyr Gly Leu Val Leu Tyr Glu Asn Lys Ala Ala Tyr Glu Arg Gln Val
85 90 95

cca cca cga gcc gtc atc aac agt gca ggc tac aaa atc ctc acg tcc	394
Pro Pro Arg Ala Val Ile Asn Ser Ala Gly Tyr Lys Ile Leu Thr Ser	
100 105 110	
gtg gac caa tac ctg gag ctc att ggc aac tcc tta cca ggg acc acg	442
Val Asp Gln Tyr Leu Glu Leu Ile Gly Asn Ser Leu Pro Gly Thr Thr	
115 120 125 130	
gca aag tgg ggc agt gcc ccc atc ctc aag tgc ccc aca cag ttc ccg	490
Ala Lys Ser Gly Ser Ala Pro Ile Leu Lys Cys Pro Thr Gln Phe Pro	
135 140 145	
ctc atc ctc tgg cat cct tat ggc cgt cac tac tac ttc tgc atg atg	538
Leu Ile Leu Trp His Pro Tyr Ala Arg His Tyr Tyr Phe Cys Met Met	
150 155 160	
aca gaa gcc gag cag gac aag tgg cag gct gtg ctg cag gac tgc atc	586
Thr Glu Ala Glu Gln Asp Lys Trp Gln Ala Val Leu Gln Asp Cys Ile	
165 170 175	
cgg cac tgc aac aat gga atc cct gag gac tcc aag gta gag ggc cct	634
Arg His Cys Asn Asn Gly Ile Pro Glu Asp Ser Lys Val Glu Gly Pro	
180 185 190	
ggc ttc aca gat gcc atc cgc atg tac cga cag tcc aag gag ctg tac	682
Ala Phe Thr Asp Ala Ile Arg Met Tyr Arg Gln Ser Lys Glu Leu Tyr	
195 200 205 210	
ggc acc tgg gag atg ctg tgt ggg aac gag gtg cag atc ctg agc aac	730
Gly Thr Trp Glu Met Leu Cys Gly Asn Glu Val Gln Ile Leu Ser Asn	
215 220 225	
ctg gtg atg gag gag ctg ggc cct gag ctg aag gca gag ctc ggc ccg	778
Leu Val Met Glu Glu Leu Gly Pro Glu Leu Lys Ala Glu Leu Gly Pro	
230 235 240	
cgg ctg aag ggg aaa ccg cag gag cgg cag cgg cag tgg atc cag atc	826
Arg Leu Lys Gly Lys Pro Gln Glu Arg Gln Arg Gln Trp Ile Gln Ile	
245 250 255	
tgg gac gcc gtg tac cac atg gtg tac gag cag gcc aag ggg cgc ttc	874
Ser Asp Ala Val Tyr His Met Val Tyr Glu Gln Ala Lys Ala Arg Phe	
260 265 270	
gag gag gtg ctg tcc aag gtg cag cag gtg cag ccg gcc atg cag gcc	922
Glu Glu Val Leu Ser Lys Val Gln Gln Val Gln Pro Ala Met Gln Ala	
275 280 285 290	
gtc atc cga act gac atg gac caa att atc acc tcc aag gag ctc ctt	970
Val Ile Arg Thr Asp Met Asp Gln Ile Ile Thr Ser Lys Glu Leu Leu	
295 300 305	
gcc agc aag atc cga gcc ttc atc ctc ccc aag gca gag gtg tgc gtg	1018
Ala Ser Lys Ile Arg Ala Phe Ile Leu Pro Lys Ala Glu Val Cys Val	
310 315 320	

egg aac cat gtc cag ccc tac atc cca tcc atc ctg gag gcc ctg atg	1066
Arg Asn His Val Gln Pro Tyr Ile Pro Ser Ile Leu Glu Ala Leu Met	
325 330 335	
gtc ccc acc agc cag gcc ttc act gag gtg cga gat gtc ttc ttc aag	1114
Val Pro Thr Ser Gln Gly Phe Thr Glu Val Arg Asp Val Phe Phe Lys	
340 345 350	
gag gtc acg gac atg aac ctg aac gtc atc aac gag gcc gcc att gac	1162
Glu Val Thr Asp Met Asn Leu Asn Val Ile Asn Glu Gly Gly Ile Asp	
355 360 365 370	
aag ctg gcc gag tac atg gag aag ctg tcc cgg ctg gcg tac cac ccc	1210
Lys Leu Gly Glu Tyr Met Glu Lys Leu Ser Arg Leu Ala Tyr His Pro	
375 380 385	
ctg aag atg cag agc tgc tat gag aag atg gag tcc ctg cga ctg gac	1258
Leu Lys Met Gln Ser Cys Tyr Glu Lys Met Glu Ser Leu Arg Leu Asp	
390 395 400	
ggg ctg cag cag cga ttt gat gtg tcc agc acg tcc gtg ttc aag cag	1306
Gly Leu Gln Gln Arg Phe Asp Val Ser Ser Thr Ser Val Phe Lys Gln	
405 410 415	
cga gcc cag atc cac atg cgg gag caa atg gac aat gcc gtg tat acg	1354
Arg Ala Gln Ile His Met Arg Glu Gln Met Asp Asn Ala Val Tyr Thr	
420 425 430	
ttc gag acc ctc ctg cac cag gag ctg ggg aag ggg ccc acc aag gag	1402
Phe Glu Thr Leu Leu His Gln Glu Leu Gly Lys Gly Pro Thr Lys Glu	
435 440 445 450	
gag ctg tgc aag tcc atc cag cgg gtc ctg gag cgg gtg ctg aaa aaa	1450
Glu Leu Cys Lys Ser Ile Gln Arg Val Leu Glu Arg Val Leu Lys Lys	
455 460 465	
tac gac tac gac agc agc tct gtg cgg aag agg ttc ttc cgg gag gcg	1498
Tyr Asp Tyr Asp Ser Ser Ser Val Arg Lys Arg Phe Phe Arg Glu Ala	
470 475 480	
ctg ctg cag atc agc atc cgg ttc ctg ctc aag aag ctg gcc cct acc	1546
Leu Leu Gln Ile Ser Ile Pro Phe Leu Leu Lys Lys Leu Ala Pro Thr	
485 490 495	
tgc aag tcc gag ctg ccc cgg ttc cag gag ctg atc ttc gag gac ttt	1594
Cys Lys Ser Glu Leu Pro Arg Phe Gln Glu Leu Ile Phe Glu Asp Phe	
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gcc agg ttc atc ctg gtg gaa aac acg tac gag gag gtg gtg ctg cag	1642
Ala Arg Phe Ile Leu Val Glu Asn Thr Tyr Glu Glu Val Val Leu Gln	
515 520 525 530	
acc gtc atg aag gac atc ctg cag gct gtg aag gag gcc gcg gtg cag	1690
Thr Val Met Lys Asp Ile Leu Gln Ala Val Lys Glu Ala Ala Val Gln	
535 540 545	

agg aag cac aac ctc tac cgg gac agc atg gtc atg cac aac agc gac	1738
Arg Lys His Asn Leu Tyr Arg Asp Ser Met Val Met His Asn Ser Asp	
550 555 560	
ccc aac ctg cac ctg ctg gcc gag ggc gcc ccc atc gac tgg ggc gag	1786
Pro Asn Leu His Leu Leu Ala Glu Gly Ala Pro Ile Asp Trp Gly Glu	
565 570 575	
gag tac agc aac agc ggc ggg ggc ggc agc ccc agc ccc agc acc ccg	1834
Glu Tyr Ser Asn Ser Gly Gly Gly Gly Ser Pro Ser Pro Ser Thr Pro	
580 585 590	
gag tca gcc acc ctc tgg gaa aag cga cgg cgc gcc aag cag gtg gtc	1882
Glu Ser Ala Thr Leu Ser Glu Lys Arg Arg Ala Lys Gln Val Val	
595 600 605 610	
tct gtg gtc cag gat gag gag gtg ggg ctg ccc ttt gag gct agc cct	1930
Ser Val Val Gln Asp Glu Glu Val Gly Leu Pro Phe Glu Ala Ser Pro	
615 620 625	
gag tca cca cca cct gcg tcc ccg gac ggt gtc act gag atc cga ggc	1978
Glu Ser Pro Pro Pro Ala Ser Pro Asp Gly Val Thr Glu Ile Arg Gly	
630 635 640	
ctg ctg gcc caa ggt ctg cgg cct gag agc ccc cca cca gcc ggc ccc	2026
Leu Leu Ala Gln Gly Leu Arg Pro Glu Ser Pro Pro Pro Ala Gly Pro	
645 650 655	
ctg ctc aac ggg gcc ccc gct ggg gag agt ccc cag cct aag gcc gcc	2074
Leu Leu Asn Gly Ala Pro Ala Gly Glu Ser Pro Gln Pro Lys Ala Ala	
660 665 670	
ccc gag gcc tcc tgg ccg cct gcc tca ccc ctc cag cat ctc ctg cct	2122
Pro Glu Ala Ser Ser Pro Pro Ala Ser Pro Leu Gln His Leu Leu Pro	
675 680 685 690	
gga aag gct gtg gac ctt ggg ccc ccc aag ccc agc gac cag gag act	2170
Gly Lys Ala Val Asp Leu Gly Pro Pro Lys Pro Ser Asp Gln Glu Thr	
695 700 705	
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Gly Glu Gln Val Ser Ser Pro Ser Ser His Pro Ala Leu His Thr Thr	
710 715 720	
acc gag gac agt gca ggg gtg cag act gag ttc taggccagtg ggtccctgac	2271
Thr Glu Asp Ser Ala Gly Val Gln Thr Glu Phe	
725 730	
tgctgcacat ggcacaggcc gttcccttcc ggacccaggc aggetcagct ctggggaggg	2331
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 <212> PRT
 <213> Homo sapiens

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 His Glu Ile Glu Gly Thr Gly Leu Pro Gln Ala Gln Leu Leu Trp Arg
 35 40 45

Lys Val Pro Leu Asp Glu Arg Ile Val Phe Ser Gly Asn Leu Phe Gln
 50 55 60
 His Gln Glu Asp Ser Lys Lys Trp Arg Asn Arg Phe Ser Leu Val Pro
 65 70 75 80
 His Asn Tyr Gly Leu Val Leu Tyr Glu Asn Lys Ala Ala Tyr Glu Arg
 85 90 95
 Gln Val Pro Pro Arg Ala Val Ile Asn Ser Ala Gly Tyr Lys Ile Leu
 100 105 110
 Thr Ser Val Asp Gln Tyr Leu Glu Leu Ile Gly Asn Ser Leu Pro Gly
 115 120 125
 Thr Thr Ala Lys Ser Gly Ser Ala Pro Ile Leu Lys Cys Pro Thr Gln
 130 135 140
 Phe Pro Leu Ile Leu Trp His Pro Tyr Ala Arg His Tyr Tyr Phe Cys
 145 150 155 160
 Met Met Thr Glu Ala Glu Gln Asp Lys Trp Gln Ala Val Leu Gln Asp
 165 170 175
 Cys Ile Arg His Cys Asn Asn Gly Ile Pro Glu Asp Ser Lys Val Glu
 180 185 190
 Gly Pro Ala Phe Thr Asp Ala Ile Arg Met Tyr Arg Gln Ser Lys Glu
 195 200 205
 Leu Tyr Gly Thr Trp Glu Met Leu Cys Gly Asn Glu Val Gln Ile Leu
 210 215 220
 Ser Asn Leu Val Met Glu Glu Leu Gly Pro Glu Leu Lys Ala Glu Leu
 225 230 235 240
 Gly Pro Arg Leu Lys Gly Lys Pro Gln Glu Arg Gln Arg Gln Trp Ile
 245 250 255
 Gln Ile Ser Asp Ala Val Tyr His Met Val Tyr Glu Gln Ala Lys Ala
 260 265 270
 Arg Phe Glu Glu Val Leu Ser Lys Val Gln Gln Val Gln Pro Ala Met
 275 280 285
 Gln Ala Val Ile Arg Thr Asp Met Asp Gln Ile Ile Thr Ser Lys Glu
 290 295 300
 Leu Leu Ala Ser Lys Ile Arg Ala Phe Ile Leu Pro Lys Ala Glu Val
 305 310 315 320
 Cys Val Arg Asn His Val Gln Pro Tyr Ile Pro Ser Ile Leu Glu Ala
 325 330 335
 Leu Met Val Pro Thr Ser Gln Gly Phe Thr Glu Val Arg Asp Val Phe
 340 345 350

Phe	Lys	Glu	Val	Thr	Asp	Met	Asn	Leu	Asn	Val	Ile	Asn	Glu	Gly	Gly		
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Ile	Asp	Lys	Leu	Gly	Glu	Tyr	Met	Glu	Lys	Leu	Ser	Arg	Leu	Ala	Tyr		
	370					375					380						
His	Pro	Leu	Lys	Met	Gln	Ser	Cys	Tyr	Glu	Lys	Met	Glu	Ser	Leu	Arg		
385					390					395					400		
Leu	Asp	Gly	Leu	Gln	Gln	Arg	Phe	Asp	Val	Ser	Ser	Thr	Ser	Val	Phe		
			405						410					415			
Lys	Gln	Arg	Ala	Gln	Ile	His	Met	Arg	Glu	Gln	Met	Asp	Asn	Ala	Val		
		420						425					430				
Tyr	Thr	Phe	Glu	Thr	Leu	Leu	His	Gln	Glu	Leu	Gly	Lys	Gly	Pro	Thr		
	435						440					445					
Lys	Glu	Glu	Leu	Cys	Lys	Ser	Ile	Gln	Arg	Val	Leu	Glu	Arg	Val	Leu		
	450					455					460						
Lys	Lys	Tyr	Asp	Tyr	Asp	Ser	Ser	Ser	Val	Arg	Lys	Arg	Phe	Phe	Arg		
465					470					475					480		
Glu	Ala	Leu	Leu	Gln	Ile	Ser	Ile	Pro	Phe	Leu	Leu	Lys	Lys	Leu	Ala		
			485						490					495			
Pro	Thr	Cys	Lys	Ser	Glu	Leu	Pro	Arg	Phe	Gln	Glu	Leu	Ile	Phe	Glu		
		500						505					510				
Asp	Phe	Ala	Arg	Phe	Ile	Leu	Val	Glu	Asn	Thr	Tyr	Glu	Glu	Val	Val		
	515						520					525					
Leu	Gln	Thr	Val	Met	Lys	Asp	Ile	Leu	Gln	Ala	Val	Lys	Glu	Ala	Ala		
	530					535					540						
Val	Gln	Arg	Lys	His	Asn	Leu	Tyr	Arg	Asp	Ser	Met	Val	Met	His	Asn		
545					550					555					560		
Ser	Asp	Pro	Asn	Leu	His	Leu	Leu	Ala	Glu	Gly	Ala	Pro	Ile	Asp	Trp		
			565						570					575			
Gly	Glu	Glu	Tyr	Ser	Asn	Ser	Gly	Gly	Gly	Gly	Ser	Pro	Ser	Pro	Ser		
		580					585						590				
Thr	Pro	Glu	Ser	Ala	Thr	Leu	Ser	Glu	Lys	Arg	Arg	Arg	Ala	Lys	Gln		
	595						600						605				
Val	Val	Ser	Val	Val	Gln	Asp	Glu	Glu	Val	Gly	Leu	Pro	Phe	Glu	Ala		
	610					615					620						
Ser	Pro	Glu	Ser	Pro	Pro	Pro	Ala	Ser	Pro	Asp	Gly	Val	Thr	Glu	Ile		
625					630					635					640		
Arg	Gly	Leu	Leu	Ala	Gln	Gly	Leu	Arg	Pro	Glu	Ser	Pro	Pro	Pro	Ala		
			645					650							655		

Gly Pro Leu Leu Asn Gly Ala Pro Ala Gly Glu Ser Pro Gln Pro Lys
 660 665 670
 Ala Ala Pro Glu Ala Ser Ser Pro Pro Ala Ser Pro Leu Gln His Leu
 675 680 685
 Leu Pro Gly Lys Ala Val Asp Leu Gly Pro Pro Lys Pro Ser Asp Gln
 690 695 700
 Glu Thr Gly Glu Gln Val Ser Ser Pro Ser Ser His Pro Ala Leu His
 705 710 715 720
 Thr Thr Thr Glu Asp Ser Ala Gly Val Gln Thr Glu Phe
 725 730

<210> 3
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Artificially
 Synthesized Primer Sequence

<400> 3
 tgtaaaacga cggccagt 18

<210> 4
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
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 Synthesized Primer Sequence

<400> 4
 accatgatta cgccaagctt g 21

<210> 5
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Artificially
 Synthesized Probe Sequence

<400> 5
 tacctggagc tcattggcaa ctctttacca 30

<210> 6
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 6
cggaattcat ggggtggatg gg 22

<210> 7
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
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Synthesized Primer Sequence

<400> 7
gcgaattcta gaactcagtc tgcacccctg c 31

<210> 8
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<212> DNA
<213> Artificial Sequence

<220>
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Synthesized Primer Sequence

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gcgaattcga actcagtctg caccctgc 29